

SEQUENCE LISTINGCDRs For FR1-H7 Amino Acid Sequences

VH (human heavy chain subclass I)

CDR1 SEQ ID NO:1	DYYMH
CDR2 SEQ ID NO:2	LVDPEDGETIYAEKFQG
CDR3 SEQ ID NO:3	DDYMDV

VL (human kappa light chain subgroup III)

CDR1 SEQ ID NO:4	RASQSVSGSALA
CDR2 SEQ ID NO:5	DASSRAT
CDR3 SEQ ID NO:6	QQYGSSPLT

Variable Region of FR1-H7 Heavy Chain

Amino Acid Sequence

SEQ ID NO:7

MAEVQLVQSGAEVKKPGASVKVSCKVSGYTFDYYMHWVQQAPGKGLEWMGLVDPEDGET  
IYAEKFQGRVTITADTSTDYAMELSSLRSEDTAVYYCARDYMDVWGKGTLVTVSSAST  
KGPVariable Region of FR1-H7 Light Chain

Amino Acid Sequence

SEQ ID NO:8

LETTLTQSPDTLSLSPGEGATLSCRASQSVSGSALAWYQQKPGQAPRLLIYDASSRATGV  
PDRFSGSGSGADFSLTISRLEPEDFAVYSCQQYGSSPLTFGPGTKVDVKRTVAAPSVFIF  
PPSDEQLKSGTASVCLLNNFYPREAKVQWKVDCDRs For FR1-A1 Amino Acid Sequences

VH (human heavy chain subclass I)

CDR1 SEQ ID NO:9	GYMH
CDR2 SEQ ID NO:10	RIIPILGIANYAQKFQG
CDR3 SEQ ID NO:11	GGDLGGMDV

VL (human kappa light chain subgroup III)

CDR1 SEQ ID NO:12	RSSQSLRHSNGYNYLD
CDR2 SEQ ID NO:13	LASNRAS
CDR3 SEQ ID NO:14	MQALQIPPT

Variable Region of FR1-A1 Heavy Chain

Amino Acid Sequences

SEQ ID NO:15.

MAQVQLVQSGAEVKKPGSSVKVSCKASGQTFTGYMHWVRQAPGQGLEWMGRIIPILGIA  
NYAQKFQGRVTITADKSTSTAYMELSSLRSEDTAVYYCARGGDLGGMDVWGQG

Variable Region of FR1-A1 Light Chain

## Amino Acid Sequences

## SEQ ID NO:16

LEIVLTQSPSLPVTTPGEPASISCRSSQSLRHSNGYNYLDWYLQKPGQSPQLLIYLASNR  
 ASGVPDRFSGSGSGTDFTLKISRVEAEDVGVYYCMQALQIPPTFGPGTKVDIKRTVAA

CDRs For FR1-4H Amino Acid Sequences

## Variable Heavy Chain

CDR1 SEQ ID NO:17           SYYS  
 CDR2 SEQ ID NO:18           YIYYSGSTNYPNPSLKS  
 CDR3 SEQ ID NO:19           EYYDSSGYFYAFDI

## Variable Light Chain]

CDR1 SEQ ID NO:20           SGSSSNIGSNYVY  
 CDR2 SEQ ID NO:21           RNNQRPS  
 CDR3 SEQ ID NO:22           AAWDDSLSGWV

Variable Region Heavy Chain FR1-4H

## Amino Acid Sequences

## SEQ ID NO:23

QVQLVEFGPGLVKPSETLSLTCTVSGGSISSYYWSWIRQPPGKGLEWIGY	50
IYYSGSTNYPNPSLKSRAISVDTSKNQFSLKLSSVTAADTAVYYCAREYY	100
YDSSGYFYAFDIWGQGTITVSS	124

Variable Region Light Chain

## Amino Acid Sequence

## SEQ ID NO:24

LPVLTQPPSASGTPGQRVSISSGSSSNIGSNYVYQQLPGTAPKLLIF	50
RNNQRPSGVPDRFSGSGSKSGTSASLAISGLRSEDEADYYCAWDDSLSGWV	100
FGGGTKLTVLG	111

CDRs For FR1-H7 Nucleic Acid Sequences

## VH (human heavy chain subclass I)

CDR1 SEQ ID NO:25   GACTACTACATGCAC  
 CDR2 SEQ ID NO:26   CTTGTTGATCCTGAAGATGGTGAAACAATCTACGCAGA  
 GAAGTTCCAGGGC  
 CDR3 SEQ ID NO:27   GATGACTACATGGACGTC

## VL (human kappa light chain subgroup III)

CDR1 SEQ ID NO:28   AGGGCCAGTCAGAGTGTTAGCGGCAGTGCGTTGGCC  
 CDR2 SEQ ID NO:29   GATGCATCCAGTAGGGCCACT  
 CDR3 SEQ ID NO:30   CAGCAATATGGTAGCTCACCTCTCACT

Variable Region of FR1-H7 Heavy Chain DNA Sequence

## SEQ ID NO:31

ATGGCCGAGGTGCAGCTGGTGCAGTCTGGGGCTGAGGTGAAGAAGCCTGGGGCCTCAGTG  
AAGGTTTCCTGCAAGGTTTCTGGATACACCTTCACCGACTACTACATGCACTGGGTGCAA  
CAGGCCCCTGGAAAAGGGCTTGAGTGGATGGGACTTGTGATCCTGAAGATGGTGAAACA  
ATCTACGCAGAGAAGTTCCAGGGCAGAGTCACCATAACCGCGGACACGTCTACAGACACA  
GCCTACATGGAGCTGAGCAGCCTGAGATCTGAGGACACGGCCGTGTATTACTGTGCGAGA  
GATGACTACATGGACGTCTGGGGCAAAGGCACCCTGGTCACCGTCTCAAGCGCCTCCACC  
AAGGGCCCA

Variable Region of FR1-H7 Light Chain DNA Sequence

SEQ ID NO:32

CTTGAAACGACACTCACGCAGTCTCCAGACACCCTGTCTTTGTCTCCAGGAGAAGGAGCC  
ACCCTCTCCTGTAGGGCCAGTCAGAGTGTTAGCGGCAGTGCGTTGGCCTGGTACCAGCAG  
AAACCTGGCCAGGCTCCCAGACTCCTCATCTATGATGCATCCAGTAGGGCCACTGGCGTC  
CCAGACAGGTTTCAGTGGCAGTGGGTCTGGGGCAGACTTCAGTCTCACCATCAGCAGACTG  
GAGCCTGAAGATTTTGCAGTGTATTCCTGTGTCAGCAATATGGTAGCTCACCTCTCACTTTC  
GGCCCTGGGACCAAAGTGGATGTCAAACGAACTGTGGCTGCACCATCTGTCTTCATCTTC  
CCGCCATCTGATGAGCAGTTGAAATCTGGAAGTGCCTCTGTTGTGTGCCTGCTGAATAAC  
TTCTATCCCAGAGAGGCCAAAGTACAGTGAAGGTGGATT

CDRs For FR1-A1 Nucleic Acid Sequences

VH (human heavy chain subclass I)

CDR1 SEQ ID NO:33 GGCTACTATATGCAC

CDR2 SEQ ID NO:34 AGGATCATCCCTATCCTTGGTATAGCAAAC  
TACGCACAGAAGTTCCAGGGC

CDR3 SEQ ID NO:35 GGAGGAGATCTGGGCGGTATGGACGTC

VL (human kappa light chain subgroup III)

CDR1 SEQ ID NO:36 AGGTCTAGTCAGAGCCTCCGGCATAGTAAT  
GGATACAACTATTTGGAT

CDR2 SEQ ID NO:37 TTGGCTTCTAATCGGGCCTCC

CDR3 SEQ ID NO:38 ATGCAAGCTCTACAAATTCCTCCGACT

Variable Region of FR1-A1 Heavy Chain

DNA Sequence

SEQ ID NO:39

ATGGCCCAGGTCCAGCTGGTGCAGTCTGGGGCTGAGGTGAAGAAGCCTGGGTCCTCGGTG  
AAGGTCTCCTGCAAGGCTTCTGGATCGACCTTCACCGGCTACTATATGCACTGGGTGCGA  
CAGGCCCCTGGACAAGGGCTTGAGTGGATGGGAAGGATCATCCCTATCCTTGGTATAGCA  
AACTACGCACAGAAGTTCCAGGGCAGAGTCACGATTACCGCGGACAAATCCACGAGCACA  
GCCTACATGGAGCTGAGCAGCCTGAGATCTGAGGACACGGCCGTGTACTACTGTGCGAGA  
GGAGGAGATCTGGGCGGTATGGACGTCTGGGGCCAAGGGA

Variable Region of FR1-A1 Light Chain

DNA Sequences

SEQ ID NO:40

CTTGAAATTGTGCTGACTCAGTCTCCACTCTCCCTGCCCCGTCACCCCTGGAGAGCCGGCC  
TCCATCTCCTGCAGGTCTAGTCAGAGCCTCCGGCATAGTAATGGATACAACCTATTTGGAT  
TGGTACCTGCAGAAGCCAGGGCAGTCTCCACAGCTCCTGATCTATTTGGCTTCTAATCGG  
GCCTCCGGGGTCCCTGACAGGTTCAGTGGCAGTGGATCAGGCACAGATTTTACACTGAAA  
ATCAGCAGAGTGGAGGCTGAGGATGTTGGGGTTTATTACTGCATGCAAGCTCTACAAATT  
CCTCCGACTTTCGGCCCTGGGACCAAAGTGGATATCAAACGAACTGTGGCTGCA

CDRs For FR1-4H Nucleic Acid Sequences

Variable Heavy Chain

CDR1 SEQ ID NO:41 AGTTACTACTGGAGC

CDR2 SEQ ID NO:42

TATATCTATTACAGTGGGAGCACCAACTACAACCCCTCCCTCAAGAGT

CDR3 SEQ ID NO:43

GAGTATTACTATGATAGTAGTGGTTATTACTTTTATGCTTTTGATATC

Variable Light Chain]

CDR1 SEQ ID NO:44 TCTGGAAGCAGCTCCAACATCGGAAGTAATTATGTATAC

CDR2 SEQ ID NO:45 AGGAATAATCAGCGGCCCTCA

CDR3 SEQ ID NO:46 GCAGCATGGGATGACAGCCTGAGTGGTTGGGTG

Variable Region Heavy Chain FR1-4H

DNA Sequences

SEQ ID NO:47

CAGGTGCAGCTGGTGGAGTTTGGCCCAGGACTGGTGAAGCCTTCGGAGAC	50
CCTGTCCCTCACCTGCACTGTCTCTGGTGGCTCCATCAGTAGTTACTACT	100
GGAGCTGGATCCGGCAGCCCCCAGGGAAGGGACTGGAGTGGATTGGGTAT	150
ATCTATTACAGTGGGAGCACCAACTACAACCCCTCCCTCAAGAGTCGAGT	200
CGCCATATCAGTAGACACGTCCAAGAACCAGTTCTCCCTGAAGCTGAGCT	250
CTGTGACCGCCGCGGACACGGCCGTGTATTACTGTGCGAGAGAGTATTAC	300
TATGATAGTAGTGGTTATTACTTTTATGCTTTTGATATCTGGGGCCAAGG	350
GACCACGGTCACCGTCTCAAGC	372

Variable Region Light Chain

DNA Sequence

SEQ ID NO:48

CTGCCTGTGCTGACTCAGCCCCCTCAGCGTCTGGGACCCCCGGGCAGAG	50
GGTCTCCATCTCTTGTCTGGAAGCAGCTCCAACATCGGAAGTAATTATG	100
TATACTGGTACCAGCAGCTCCCAGGAACGGCCCCCAAACCTCCTCATCTTT	150
AGGAATAATCAGCGGCCCTCAGGGGTCCCTGACCGATTCTCTGGCTCCAA	200
GTCTGGCACTTCAGCCTCCCTGGCCATCAGTGGGCTCCGGTCCGAGGATG	250
AGGCTGATTATTACTGTGCAGCATGGGATGACAGCCTGAGTGGTTGGGTG	300
TCGGCGGAGGGACCAAGCTGACCGTCCTAGGT	333